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Scientific and Technical Information Center

DEC 13 2005

SEARCH REQUEST FORM

Requester's Full Name: TANE ZARA Examiner #: 77512 Date: 12-13-05
 Art Unit: 1635 Phone Number: 2-0765 Serial Number: 091296 264
 Location (Bldg/Room#): 2D28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following: **MG**

Title of Invention: Neuropilin

Inventors (please provide full names): Wright et al.

Earliest Priority Date: 4-23-99

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos

1-3, 5, 6, 8-12

length minimum 20 NT.

length max. 100 NTS.

include
Interference
PLEASE.

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____ NA Sequence (#)

_____ STN _____ Dialog

Searcher Phone #: _____ AA Sequence (#)

_____ Questel/Orbit _____ Lexis/Nexis

Searcher Location: _____ Structure (#)

_____ Westlaw _____ WWW/Internet

Date Searcher Picked Up: _____ Bibliographic

_____ In-house sequence systems

Date Completed: _____ Litigation

_____ Commercial _____ Oligomer _____ Score/Length
 _____ Interference _____ SPDI _____ Encoder/Transl
 _____ Other (specify)

Searcher Prep & Review Time: _____ Fulltext

Online Time: _____ Other

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds

(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-1

Sequence: 1 gagcgcagcccccctcca 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Title: US-09-296-264-2

Perfect score: 20
Sequence: 1 cgagcagcgcgacagagagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

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Minimum DB seq length: 20
Maximum DB seq length: 100
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents NA New:*

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4  /cgn2_6/prodata/2/pna/us09 NEW COMB seq.*
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6  /cgn2_6/prodata/2/pna/us11 NEW COMB seq.*
7  /cgn2_6/prodata/2/pna/us11 NEW COMB seq.*
8  /cgn2_6/prodata/2/pna/us11 NEW COMB seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcagcgagcgagcgagc 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending Patents NA Main:*

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- 83: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds

(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20
Sequence: 1 ggacgagggcgagcagcgcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-3
Perfect score: 20
Sequence: 1 59acgagggcagcagcgcg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_NA_Main:*
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41: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*

44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US105_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US107F_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US107G_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US109D_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US604A_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US604B_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US605_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US606_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Tue Jan 3 11:52:56 2006

US-09-296-264-5. sz20-100.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds

(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20
Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds

(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-5
Perfect score: 20
Sequence: 1 ttcttcagggaatccg9999 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_NA_Main:*

- 1: /cgn2_6/prodata/1/pna/PCRTUSA_COMB.seq:*
- 2: /cgn2_6/prodata/1/pna/PCRTUSC_COMB.seq:*
- 3: /cgn2_6/prodata/1/pna/PCRTUSC_COMB.seq:*
- 4: /cgn2_6/prodata/1/pna/US075_COMB.seq:*
- 5: /cgn2_6/prodata/1/pna/US075_COMB.seq:*
- 6: /cgn2_6/prodata/1/pna/US076_COMB.seq:*
- 7: /cgn2_6/prodata/1/pna/US076_COMB.seq:*
- 8: /cgn2_6/prodata/1/pna/US078_COMB.seq:*
- 9: /cgn2_6/prodata/1/pna/US079_COMB.seq:*
- 10: /cgn2_6/prodata/1/pna/US080_COMB.seq:*
- 11: /cgn2_6/prodata/1/pna/US081_COMB.seq:*
- 12: /cgn2_6/prodata/1/pna/US082_COMB.seq:*
- 13: /cgn2_6/prodata/1/pna/US083_COMB.seq:*
- 14: /cgn2_6/prodata/1/pna/US084_COMB.seq:*
- 15: /cgn2_6/prodata/1/pna/US085_COMB.seq:*
- 16: /cgn2_6/prodata/1/pna/US086_COMB.seq:*
- 17: /cgn2_6/prodata/1/pna/US087_COMB.seq:*
- 18: /cgn2_6/prodata/1/pna/US088_COMB.seq:*
- 19: /cgn2_6/prodata/1/pna/US089_COMB.seq:*
- 20: /cgn2_6/prodata/1/pna/US090_COMB.seq:*
- 21: /cgn2_6/prodata/1/pna/US091_COMB.seq:*
- 22: /cgn2_6/prodata/1/pna/US092_COMB.seq:*
- 23: /cgn2_6/prodata/1/pna/US093_COMB.seq:*
- 24: /cgn2_6/prodata/1/pna/US094_COMB.seq:*
- 25: /cgn2_6/prodata/1/pna/US095_COMB.seq:*
- 26: /cgn2_6/prodata/1/pna/US096_COMB.seq:*
- 27: /cgn2_6/prodata/1/pna/US097_COMB.seq:*
- 28: /cgn2_6/prodata/1/pna/US098_COMB.seq:*
- 29: /cgn2_6/prodata/1/pna/US099_COMB.seq:*
- 30: /cgn2_6/prodata/1/pna/US100_COMB.seq:*
- 31: /cgn2_6/prodata/1/pna/US101_COMB.seq:*
- 32: /cgn2_6/prodata/1/pna/US102_COMB.seq:*
- 33: /cgn2_6/prodata/1/pna/US103_COMB.seq:*
- 34: /cgn2_6/prodata/1/pna/US104_COMB.seq:*
- 35: /cgn2_6/prodata/1/pna/US105_COMB.seq:*
- 36: /cgn2_6/prodata/1/pna/US106_COMB.seq:*
- 37: /cgn2_6/prodata/1/pna/US107_COMB.seq:*
- 38: /cgn2_6/prodata/1/pna/US108_COMB.seq:*
- 39: /cgn2_6/prodata/1/pna/US109_COMB.seq:*
- 40: /cgn2_6/prodata/1/pna/US110_COMB.seq:*
- 41: /cgn2_6/prodata/1/pna/US111_COMB.seq:*
- 42: /cgn2_6/prodata/1/pna/US112_COMB.seq:*
- 43: /cgn2_6/prodata/1/pna/US113_COMB.seq:*

- 44: /cgn2_6/prodata/1/pna/US102B_COMB.seq:*
- 45: /cgn2_6/prodata/1/pna/US103A_COMB.seq:*
- 46: /cgn2_6/prodata/1/pna/US103B_COMB.seq:*
- 47: /cgn2_6/prodata/1/pna/US103C_COMB.seq:*
- 48: /cgn2_6/prodata/1/pna/US103D_COMB.seq:*
- 49: /cgn2_6/prodata/1/pna/US103E_COMB.seq:*
- 50: /cgn2_6/prodata/1/pna/US103F_COMB.seq:*
- 51: /cgn2_6/prodata/1/pna/US104_COMB.seq:*
- 52: /cgn2_6/prodata/1/pna/US105_COMB.seq:*
- 53: /cgn2_6/prodata/1/pna/US106A_COMB.seq:*
- 54: /cgn2_6/prodata/1/pna/US106B_COMB.seq:*
- 55: /cgn2_6/prodata/1/pna/US107A_COMB.seq:*
- 56: /cgn2_6/prodata/1/pna/US107B_COMB.seq:*
- 57: /cgn2_6/prodata/1/pna/US107C_COMB.seq:*
- 58: /cgn2_6/prodata/1/pna/US107D_COMB.seq:*
- 59: /cgn2_6/prodata/1/pna/US107E_COMB.seq:*
- 60: /cgn2_6/prodata/1/pna/US107F_COMB.seq:*
- 61: /cgn2_6/prodata/1/pna/US107G_COMB.seq:*
- 62: /cgn2_6/prodata/1/pna/US108_COMB.seq:*
- 63: /cgn2_6/prodata/1/pna/US109A_COMB.seq:*
- 64: /cgn2_6/prodata/1/pna/US109B_COMB.seq:*
- 65: /cgn2_6/prodata/1/pna/US109C_COMB.seq:*
- 66: /cgn2_6/prodata/1/pna/US110A_COMB.seq:*
- 67: /cgn2_6/prodata/1/pna/US110B_COMB.seq:*
- 68: /cgn2_6/prodata/1/pna/US110C_COMB.seq:*
- 69: /cgn2_6/prodata/1/pna/US110D_COMB.seq:*
- 70: /cgn2_6/prodata/1/pna/US111A_COMB.seq:*
- 71: /cgn2_6/prodata/1/pna/US111B_COMB.seq:*
- 72: /cgn2_6/prodata/1/pna/US112_COMB.seq:*
- 73: /cgn2_6/prodata/1/pna/US117_COMB.seq:*
- 74: /cgn2_6/prodata/1/pna/US600_COMB.seq:*
- 75: /cgn2_6/prodata/1/pna/US601_COMB.seq:*
- 76: /cgn2_6/prodata/1/pna/US602A_COMB.seq:*
- 77: /cgn2_6/prodata/1/pna/US602B_COMB.seq:*
- 78: /cgn2_6/prodata/1/pna/US603_COMB.seq:*
- 79: /cgn2_6/prodata/1/pna/US604A_COMB.seq:*
- 80: /cgn2_6/prodata/1/pna/US604B_COMB.seq:*
- 81: /cgn2_6/prodata/1/pna/US605_COMB.seq:*
- 82: /cgn2_6/prodata/1/pna/US606_COMB.seq:*
- 83: /cgn2_6/prodata/1/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

Tue Jan 3 11:52:57 2006

US-09-296-264-6.sz20-100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds
(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 99gtagtcagcg99agcg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-6
Perfect score: 20
Sequence: 1 999tagtcagcgagcg 20

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 2765789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending Patents NA Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US076_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US079_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US104A_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US105A_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US105B_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US107F_COMB.seq:*
- 61: /cgn2_6/ptodata/1/pna/US107G_COMB.seq:*
- 62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
- 63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
- 64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
- 65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
- 66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:*
- 67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:*
- 68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:*
- 69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:*
- 70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:*
- 71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:*
- 72: /cgn2_6/ptodata/1/pna/US117_COMB.seq:*
- 73: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
- 74: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
- 75: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:*
- 76: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:*
- 77: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*
- 78: /cgn2_6/ptodata/1/pna/US604_COMB.seq:*
- 79: /cgn2_6/ptodata/1/pna/US604B_COMB.seq:*
- 80: /cgn2_6/ptodata/1/pna/US605_COMB.seq:*
- 81: /cgn2_6/ptodata/1/pna/US606_COMB.seq:*
- 82: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*
- 83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtccaccagcagcagctg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Pending Patents NA Main:*

1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/PCTUSB_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
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9: /cgn2_6/ptodata/1/pna/US07_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
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12: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
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15: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
16: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
17: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
18: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
19: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
25: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
26: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
27: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
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34: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
36: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
39: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US09_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq.*

44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq.*
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq.*
46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq.*
48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq.*
49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq.*
50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq.*
51: /cgn2_6/ptodata/1/pna/US103G_COMB.seq.*
52: /cgn2_6/ptodata/1/pna/US103H_COMB.seq.*
53: /cgn2_6/ptodata/1/pna/US103I_COMB.seq.*
54: /cgn2_6/ptodata/1/pna/US103J_COMB.seq.*
55: /cgn2_6/ptodata/1/pna/US103K_COMB.seq.*
56: /cgn2_6/ptodata/1/pna/US103L_COMB.seq.*
57: /cgn2_6/ptodata/1/pna/US103M_COMB.seq.*
58: /cgn2_6/ptodata/1/pna/US103N_COMB.seq.*
59: /cgn2_6/ptodata/1/pna/US103O_COMB.seq.*
60: /cgn2_6/ptodata/1/pna/US103P_COMB.seq.*
61: /cgn2_6/ptodata/1/pna/US103Q_COMB.seq.*
62: /cgn2_6/ptodata/1/pna/US103R_COMB.seq.*
63: /cgn2_6/ptodata/1/pna/US103S_COMB.seq.*
64: /cgn2_6/ptodata/1/pna/US103T_COMB.seq.*
65: /cgn2_6/ptodata/1/pna/US103U_COMB.seq.*
66: /cgn2_6/ptodata/1/pna/US103V_COMB.seq.*
67: /cgn2_6/ptodata/1/pna/US103W_COMB.seq.*
68: /cgn2_6/ptodata/1/pna/US103X_COMB.seq.*
69: /cgn2_6/ptodata/1/pna/US103Y_COMB.seq.*
70: /cgn2_6/ptodata/1/pna/US103Z_COMB.seq.*
71: /cgn2_6/ptodata/1/pna/US104A_COMB.seq.*
72: /cgn2_6/ptodata/1/pna/US104B_COMB.seq.*
73: /cgn2_6/ptodata/1/pna/US104C_COMB.seq.*
74: /cgn2_6/ptodata/1/pna/US104D_COMB.seq.*
75: /cgn2_6/ptodata/1/pna/US104E_COMB.seq.*
76: /cgn2_6/ptodata/1/pna/US104F_COMB.seq.*
77: /cgn2_6/ptodata/1/pna/US104G_COMB.seq.*
78: /cgn2_6/ptodata/1/pna/US104H_COMB.seq.*
79: /cgn2_6/ptodata/1/pna/US104I_COMB.seq.*
80: /cgn2_6/ptodata/1/pna/US104J_COMB.seq.*
81: /cgn2_6/ptodata/1/pna/US104K_COMB.seq.*
82: /cgn2_6/ptodata/1/pna/US104L_COMB.seq.*
83: /cgn2_6/ptodata/1/pna/US104M_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

US-09-296-264-9.BZ20-100.

OM nucleic - nucleic search, using sw model

Title: US-09-296-264-9

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

```
Minimum DB seq length: 20
Maximum DB seq length: 100
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending Patents NA New.*

- 1 : /cgn2_6/ptodata/2/pna/PCT NEW COMB. seg.*
- 2 : /cgn2_6/ptodata/2/pna/US06 NEW COMB. seg.*
- 3 : /cgn2_6/ptodata/2/pna/US07 NEW COMB. seg.*
- 4 : /cgn2_6/ptodata/2/pna/US08 NEW COMB. seg.*
- 5 : /cgn2_6/ptodata/2/pna/US09 NEW COMB. seg.*
- 6 : /cgn2_6/ptodata/2/pna/US10 NEW COMB. seg.*
- 7 : /cgn2_6/ptodata/2/pna/US11 NEW COMB. seg.*
- 8 : /cgn2_6/ptodata/2/pna/US61 NEW COMB. seg.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Results

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tgaagtcgcgggtggaagtcg 20

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100 ;

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
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- 22: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
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- 27: /cgn2_6/ptodata/1/pna/US095_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US095_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US097_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 39: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
- 40: /cgn2_6/ptodata/1/pna/US100_COMB.seq:*
- 41: /cgn2_6/ptodata/1/pna/US100_COMB.seq:*
- 42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
- 43: /cgn2_6/ptodata/1/pna/US102_COMB.seq:*

- 44: /cgn2_6/ptodata/1/pna/US102_COMB.seq:*
- 45: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 46: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 47: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 48: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 49: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 50: /cgn2_6/ptodata/1/pna/US103_COMB.seq:*
- 51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
- 52: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
- 53: /cgn2_6/ptodata/1/pna/US106_COMB.seq:*
- 54: /cgn2_6/ptodata/1/pna/US106_COMB.seq:*
- 55: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 56: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 57: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 58: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 59: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 60: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 61: /cgn2_6/ptodata/1/pna/US107_COMB.seq:*
- 62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
- 63: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
- 64: /cgn2_6/ptodata/1/pna/US109_COMB.seq:*
- 65: /cgn2_6/ptodata/1/pna/US109_COMB.seq:*
- 66: /cgn2_6/ptodata/1/pna/US109_COMB.seq:*
- 67: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 68: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 69: /cgn2_6/ptodata/1/pna/US110_COMB.seq:*
- 70: /cgn2_6/ptodata/1/pna/US111_COMB.seq:*
- 71: /cgn2_6/ptodata/1/pna/US111_COMB.seq:*
- 72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:*
- 73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:*
- 74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
- 75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
- 76: /cgn2_6/ptodata/1/pna/US602_COMB.seq:*
- 77: /cgn2_6/ptodata/1/pna/US602_COMB.seq:*
- 78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*
- 79: /cgn2_6/ptodata/1/pna/US604_COMB.seq:*
- 80: /cgn2_6/ptodata/1/pna/US604_COMB.seq:*
- 81: /cgn2_6/ptodata/1/pna/US605_COMB.seq:*
- 82: /cgn2_6/ptodata/1/pna/US606_COMB.seq:*
- 83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds
(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20
Sequence: 1 gtgcgcgacgtggaccaccaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query
------------	-------	-------

Tue Jan 3 11:52:52 2006

US-09-296-264-11. sz20-100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds
(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID
No.					

Description

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357.539 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 1 gfgcgcagctgagaccaga 20

Sequence: IDENTITY_NTUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA Main:*

- 1: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 9: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 10: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 11: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 13: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 15: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 24: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 26: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 27: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 28: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 29: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 30: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 31: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 32: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 33: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 34: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 35: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 36: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 37: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 38: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
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- 40: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 41: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 42: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
- 43: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*

- 44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq.*
- 45: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 47: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 48: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 49: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 50: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 51: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 52: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 53: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 54: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 55: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 56: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 57: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 58: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 59: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 60: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 61: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 62: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 63: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 64: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 65: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 66: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 67: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 68: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 69: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 70: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 71: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 72: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 73: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 74: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 76: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 77: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 78: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 79: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 80: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 81: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 82: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
- 83: /cgn2_6/ptodata/1/pna/US103B_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Tue Jan 3 11:52:53 2006

us-09-296-264-12.sz20-100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 / Search time 33.9 Seconds
(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 CGACCCACAGACAGCCCC 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:00:26 ; Search time 3092.9 Seconds
(without alignments)
357,539 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 cgacccacagacagcccc 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 53376892

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUSA COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUSB COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUSC COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06 COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US075 COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US076 COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US077 COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US078 COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US079 COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US080 COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US081 COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US082 COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US083 COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US084 COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US085 COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US086 COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US087 COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US088 COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US089 COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US090 COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US091 COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US092 COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US093 COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US094 COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US095A COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US095B COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US095C COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096A COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US096B COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US096C COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US097A COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US097B COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098A COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US098B COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099A COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099B COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099C COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US099D COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US099E COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US100A COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US100B COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US101 COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102A COMB.seq:*

44: /cgn2_6/ptodata/1/pna/US102B COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US103A COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US103B COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US103C COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US103D COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US103E COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US103F COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US104 COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US105 COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US106A COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US106B COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US107A COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US107B COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US107C COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US107D COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US107E COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US107F COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US107G COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US108 COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US109A COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US109B COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US109C COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US110A COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US110B COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US110C COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US110D COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US111A COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US111B COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US117 COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US117 COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US600 COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US601 COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US602A COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US602B COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US603 COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US604A COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US604B COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US605 COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US606 COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US607 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 12:29:21 ; Search time 33.9 Seconds
(without alignments)
202.866 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20
Sequence: 1 gagcgcgcagcccccctccca 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 890530 seqs, 171929046 residues

Total number of hits satisfying chosen parameters: 1590298

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents NA New: *
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq: *
8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result